

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
 Hillman, Jennifer L.
 Guegler, Karl J.
 Corley, Neil C.
 Baughn, Mariah R.
 Azimzai, Yalda

(ii) TITLE OF THE INVENTION: HUMAN UBIQUITIN-CONJUGATING ENZYME
 HOMOLOGS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Drive
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
 (B) FILING DATE: HERewith
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C
 (B) REGISTRATION NUMBER: 39,132
 (C) REFERENCE/DOCKET NUMBER: PF-0502 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT14
 (B) CLONE: 1728211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Ala Leu Leu Ala Thr Ser Leu Pro Glu Gly Ile Met Val Lys
 5 10 15

09930026-081401

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Phe | Glu | Asp | Arg | Met | Asp | Leu | Phe | Ser | Ala | Leu | Ile | Lys | Gly | |
| | | | | 20 | | | | | 25 | | | | | 30 | |
| Pro | Thr | Arg | Thr | Pro | Tyr | Glu | Asp | Gly | Leu | Tyr | Leu | Phe | Asp | Ile | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| Gln | Leu | Pro | Asn | Ile | Tyr | Pro | Ala | Val | Pro | Pro | His | Phe | Cys | Tyr | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Leu | Ser | Gln | Cys | Ser | Gly | Arg | Leu | Asn | Pro | Asn | Leu | Tyr | Asp | Asn | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Gly | Lys | Val | Cys | Val | Ser | Leu | Leu | Gly | Thr | Trp | Ile | Gly | Lys | Gly | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Thr | Glu | Arg | Trp | Thr | Ser | Lys | Ser | Ser | Leu | Leu | Gln | Val | Leu | Ile | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Ser | Ile | Gln | Gly | Leu | Ile | Leu | Val | Asn | Glu | Pro | Tyr | Tyr | Asn | Glu | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Ala | Gly | Phe | Asp | Ser | Asp | Arg | Gly | Leu | Gln | Glu | Gly | Tyr | Glu | Asn | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Ser | Arg | Cys | Tyr | Asn | Glu | Met | Ala | Leu | Ile | Arg | Val | Val | Gln | Ser | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Met | Thr | Gln | Leu | Val | Arg | Arg | Pro | Pro | Glu | Val | Phe | Glu | Gln | Glu | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Ile | Arg | Gln | His | Phe | Ser | Thr | Gly | Gly | Trp | Arg | Leu | Val | Asn | Arg | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Ile | Glu | Ser | Trp | Leu | Glu | Thr | His | Ala | Leu | Leu | Glu | Lys | Ala | Gln | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Ala | Leu | Pro | Asn | Gly | Val | Pro | Lys | Ala | Ser | Ser | Ser | Pro | Glu | Pro | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Pro | Ala | Val | Ala | Glu | Leu | Ser | Asp | Ser | Gly | Gln | Gln | Glu | Pro | Glu | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Asp | Gly | Gly | Pro | Ala | Pro | Gly | Glu | Ala | Ser | Gln | Gly | Ser | Asp | Ser | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Glu | Gly | Gly | Ala | Gln | Gly | Leu | Ala | Phe | Ser | | | | | | |
| | | | | 245 | | | | | 250 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINTNOT13
- (B) CLONE: 1803905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gln | Gln | Gln | Met | Thr | Ser | Ser | Gln | Lys | Ala | Leu | Met | Leu | |
| | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Leu | Lys | Ser | Leu | Gln | Glu | Glu | Pro | Val | Glu | Gly | Phe | Arg | Ile | |
| | | | | 20 | | | | | 25 | | | | | 30 | |
| Thr | Leu | Val | Asp | Glu | Ser | Asp | Leu | Tyr | Asn | Trp | Glu | Val | Ala | Ile | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| Phe | Gly | Leu | Pro | Asn | Thr | Leu | Tyr | Glu | Gly | Gly | Tyr | Phe | Lys | Ala | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| His | Ile | Lys | Phe | Pro | Ile | Asp | Tyr | Pro | Tyr | Ser | Pro | Pro | Thr | Phe | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Arg | Phe | Leu | Thr | Lys | Met | Trp | His | Pro | Asn | Ile | Tyr | Glu | Asn | Gly | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Asp | Val | Cys | Ile | Ser | Ile | Leu | His | Pro | Pro | Val | Asp | Asp | Pro | Gln | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Ser | Gly | Glu | Leu | Pro | Ser | Glu | Arg | Trp | Asn | Pro | Thr | Gln | Asn | Val | |
| | | | | 110 | | | | | 115 | | | | | 120 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Thr | Ile | Leu | Leu | Ser | Val | Ile | Ser | Leu | Leu | Asn | Glu | Pro | Asn | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Thr | Phe | Ser | Pro | Ala | Asn | Val | Asp | Ala | Ser | Val | Met | Phe | Arg | Lys | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Trp | Arg | Asp | Ser | Lys | Gly | Lys | Asp | Lys | Glu | Tyr | Ala | Glu | Ile | Ile | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Arg | Lys | Gln | Val | Ser | Ala | Thr | Lys | Ala | Glu | Ala | Glu | Lys | Asp | Gly | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Val | Lys | Val | Pro | Thr | Thr | Leu | Ala | Glu | Tyr | Cys | Ile | Lys | Thr | Lys | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Val | Pro | Ser | Asn | Asp | Asn | Ser | Ser | Asp | Leu | Leu | Tyr | Asp | Asp | Leu | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Tyr | Asp | Asp | Asp | Ile | Asp | Asp | Glu | Asp | Glu | Glu | Glu | Glu | Asp | Ala | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Asp | Cys | Tyr | Asp | Asp | Asp | Asp | Ser | Gly | Met | Arg | Ser | Arg | Asp | Val | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Leu | Gln | Cys | Pro | Cys | Thr | Ala | Leu | Pro | Ser | Gln | Ala | Lys | Gly | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Arg | Gly | Ala | Ser | Gly | Asp | Leu | Ala | Met | Ala | Pro | Gln | Gln | Lys | Pro | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Ile | His | Ser | Gly | Trp | Gly | Asn | Thr | His | Ser | Ser | Cys | | | | |
| | | | | 275 | | | | | 280 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT16
- (B) CLONE: 2792472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Thr | Arg | Tyr | Asn | Leu | Lys | Ser | Pro | Ala | Val | Lys | Arg | Leu | |
| | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | Lys | Glu | Ala | Ala | Glu | Leu | Lys | Asp | Pro | Thr | Asp | His | Tyr | His | |
| | | | | 20 | | | | | 25 | | | | | 30 | |
| Ala | Gln | Pro | Leu | Glu | Asp | Asn | Leu | Phe | Glu | Trp | His | Phe | Thr | Val | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| Arg | Gly | Pro | Pro | Asp | Ser | Asp | Phe | Asp | Gly | Gly | Val | Tyr | His | Gly | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Arg | Ile | Val | Leu | Pro | Pro | Glu | Tyr | Pro | Met | Lys | Pro | Pro | Ser | Ile | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Ile | Leu | Leu | Thr | Ala | Asn | Gly | Arg | Phe | Glu | Val | Gly | Lys | Lys | Ile | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Cys | Leu | Ser | Ile | Ser | Gly | His | His | Pro | Glu | Thr | Trp | Gln | Pro | Ser | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Trp | Ser | Ile | Arg | Thr | Ala | Leu | Leu | Ala | Ile | Ile | Gly | Phe | Met | Pro | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Thr | Lys | Gly | Glu | Gly | Ala | Ile | Gly | Ser | Leu | Asp | Tyr | Thr | Pro | Glu | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Glu | Arg | Arg | Ala | Leu | Ala | Lys | Lys | Ser | Gln | Asp | Phe | Cys | Cys | Glu | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Gly | Cys | Gly | Ser | Ala | Met | Lys | Asp | Val | Leu | Leu | Pro | Leu | Lys | Ser | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Gly | Ser | Asp | Ser | Ser | Gln | Ala | Asp | Gln | Glu | Ala | Lys | Glu | Leu | Ala | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Arg | Gln | Ile | Ser | Phe | Lys | Ala | Glu | Val | Asn | Ser | Ser | Gly | Lys | Thr | |
| | | | | 185 | | | | | 190 | | | | | 195 | |

| | | | |
|---|-----|-----|-----|
| Ile Ser Glu Ser Asp Leu Asn His Ser Phe Ser Leu Thr Asp Leu | 200 | 205 | 210 |
| Gln Asp Asp Ile Pro Thr Thr Phe Gln Gly Ala Thr Ala Ser Thr | 215 | 220 | 225 |
| Ser Tyr Gly Leu Gln Asn Ser Ser Ala Ala Ser Phe His Gln Pro | 230 | 235 | 240 |
| Thr Gln Pro Val Ala Lys Asn Thr Ser Met Ser Pro Arg Gln Arg | 245 | 250 | 255 |
| Arg Ala Gln Gln Gln Ser Gln Arg Arg Leu Ser Thr Ser Pro Asp | 260 | 265 | 270 |
| Val Ile Gln Gly His Gln Pro Arg Asp Asn His Thr Asp His Gly | 275 | 280 | 285 |
| Gly Ser Ala Val Leu Ile Val Ile Leu Thr Leu Ala Leu Ala Ala | 290 | 295 | 300 |
| Leu Ile Phe Arg Arg Ile Tyr Leu Ala Asn Glu Tyr Ile Phe Asp | 305 | 310 | 315 |
| Phe Glu Leu | | | |

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT14
- (B) CLONE: 1728211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AGGTCTTCTC | CGTACTGGAG | TTTGCACCCT | CAAATCATTC | TTTTAAGAAA | ATTGAGTTCC | 60 |
| AGCCTCCAGA | AGCCAAGAAG | TTCTTCAGCA | CAGTGCGGAA | GGAGATGGCG | CTGCTGGCTA | 120 |
| CCTCACTGCC | TGAGGGCATC | ATGGTCAAGA | CTTTTGAAGA | TAGAATGGAC | CTCTTCTCAG | 180 |
| CTCTCATCAA | GGGCCCCACT | CGAACCCCT | ACGAGGATGG | CCTCTACTTG | TTTGACATCC | 240 |
| AGCTCCCCAA | CATCTACCCA | GCCGTGCCCC | CCCACTTCTG | CTACCTCTCC | CAATGCAGTG | 300 |
| GCCGCCTGAA | CCCCAACCTG | TATGACAATG | GGAAGGTGTG | TGTCAGCCTC | CTGGGCACCT | 360 |
| GGATTGGAAA | GGGGACAGAG | AGGTGGACAA | GCAAGTCCAG | CCTTCTCCAG | GTGCTCATCT | 420 |
| CCATCCAAGG | TCTGATCCTG | GTAAATGAAC | CATACTACAA | CGAAGCCGGC | TTCGACAGTG | 480 |
| ACCGAGGCCT | GCAGGAAGGC | TATGAAAACA | GTGCTGTGTA | CAATGAGATG | GCGCTGATCC | 540 |
| GCGTGGTGCA | GTCCATGACC | CAGCTGGTGC | GGCGGCCCCC | CGAGGTCTTT | GAGCAGGAGA | 600 |
| TCAGGCAACA | CTTTAGCACT | GCTGGCTGGC | GGCTGGTGAA | CCGTATCGAG | TCCTGGCTGG | 660 |
| AAACCCATGC | CCTGCTGGAG | AAGGCCCAGG | CACTGCCCAA | CGGGGTGCCC | AAGGCCAGCA | 720 |
| GCTCGCCAGA | GCCCCCAGCT | GTAGCCGAGC | TGTCAGACTC | CGGCCAACAA | GAACCTGAGG | 780 |
| ATGGAGGGCC | AGCCCCAGGA | GAGGCCTCCC | AGGGCTCAGA | CTCAGAGGGC | GGTGCCGAGG | 840 |
| GCCTGGCCTT | CAGCTAGCAG | GGACCACACA | GACCAGACTT | CGGAGACCGC | ACCAGACGCA | 900 |
| TCGGTGCCAC | CCAGTGTGAA | ACCCAAAGAA | GCGGAGAAAG | AGCNTTAAGA | GCTACCGGAG | 960 |
| CTTCTTACCT | GAGAAGAGTG | GCTACCCTGA | CATCGGCTTC | CCCCTC | | 1006 |

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINTNOT13
- (B) CLONE: 1803905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| TTTNTGTGT | GTGCNCCNG | TNNGTGNC | TNCTANGTG | TGGGNTTGT | TGTNGGTGTC | 60 |
| TTCTCTGTT | TNTNTTNC | TTGCCATTG | CTCAGNCTC | CNGTCCTCN | NNNCCNNTT | 120 |
| TGNGCNCCCC | CCNATGTCC | TGCGCCCTAG | NNGTTTGGN | CNCCCCAAA | GNTCTCNGC | 180 |
| CTNNCTGAAA | GGGNNCCCC | CTNNGAAAAG | GCCTNCTCG | NAATTGGNG | AAAAANATC | 240 |
| CCCNTNGCCA | AGGGNNGGNG | GGGAAAACCC | CGGGTTTNG | AAAGGGGGCN | TTTTNCCGNG | 300 |
| GNNATTNCCC | CCCCGTGTG | GTNTGGNACC | GGNNTTCCCC | NGANCCTNT | TTAACNAANC | 360 |
| TTGGGGGAAG | GTTTNNCCAA | NTTNTTTCG | GACTTCCCC | CAACACNCN | TTTANNGGAA | 420 |
| NGGCGNCNT | ATTTCTTCG | CCGAGGGTA | CATTCTGAT | TTGGAGCGCC | GCCGCCGCGA | 480 |
| TGGCCAGCA | GCAGATGACC | AGCTCGCAGA | AGGCCCTGAT | GCTCGAGCTG | AAATCCCTGC | 540 |
| AGGAGGAACC | GGTGGAGGGC | TTCCGGATCA | CCCTGGTGGA | CGAGTCCGAC | CTCTACAACT | 600 |
| GGGAGGTGGC | CATCTTCGGA | CTCCCCAACA | CCCTCTACGA | AGGCGGCTAC | TTCAAGGCGC | 660 |
| ATATTAAATT | TCCTATTGAC | TACCCCTATT | CACCACCTAC | CTTCAGATT | TTGACCAAAA | 720 |
| TGTGGCACC | CAACATTTAT | GAGAATGGAG | ATGTATGCAT | TTCGATTCTT | CATCCGCCTG | 780 |
| TAGATGACCC | ACAGAGTGGA | GAAGTGCCT | CTGAAAGGTG | GAATCCTACT | CAGAATGTGA | 840 |
| GGACTATCCT | ATTAAGTGTA | ATCTCACTGC | TTAATGAGCC | CAACACCTTC | TCCCCAGCCA | 900 |
| ATGTCGATGC | TTCAGTTATG | TTCAGGAAAT | GGAGAGACAG | TAAAGGAAAA | GACAAAGAAT | 960 |
| ATGCTGAAAT | TATTAGGAAA | CAAGTTTCAG | CCACTAAGGC | CGAAGCAGAA | AAGGATGGAG | 1020 |
| TGAAGGTCCC | CACAACCCTG | GCGGAATACT | GCATCAAAAC | TAAAGTGCCT | TCCAATGACA | 1080 |
| ACAGCTCAGA | TTTGCTTTAC | GACGACTTGT | ATGATGACGA | CATTGATGAT | GAAGATGAGG | 1140 |
| AGGAGGAAGA | TGCCGACTGT | TATGATGATG | ATGATTCTGG | GATGAGGAGT | CGTGACGTGC | 1200 |
| TCCTTCAGTG | CCCCGTGACT | GCCCTGCCAT | CTCAGGCCAA | AGGGAGGGGA | GCAAGTGGGG | 1260 |
| ACCTGGCCAT | GGCCCCTCAG | CAAAAACCTA | TTCACAGCGG | GTGGGGAAAC | ACACACAGCT | 1320 |
| CCTGCTGACT | CCCCTTATGG | ATCTCAGTTT | GCTCCTTTTT | ATGGACCTTT | AATGGAGAGA | 1380 |
| GAGTAACCTT | CCACAGAAAT | TCTGAATTCT | TGCATTCTTT | ACCTTCCAT | CACATATATT | 1440 |
| ATTCTTTTTT | TAAAAATAT | GAACCCAAAC | TCCCGCCTCA | CTTCGTCCT | ACAGAATGTT | 1500 |
| CACAGCAAAA | CACGTTTGGT | CTGTTTTTAG | ATTCTTGAAG | AATTCAATAG | TCTTTCAAGA | 1560 |
| TGTTTAATGT | GTTTAAAGCT | GGGAACCTGT | TGGGAGTTCA | CAAGTGCTGC | ATATACTGGG | 1620 |
| TAGCAAAAGA | AAATGGAAAA | AAACCCACAA | AACAACTTT | AAAAAAAAAA | AAAAACAAAT | 1680 |
| TTGCCAAGGT | TTAGCTGCTC | ATTTACATTA | GTGTGTGTGC | ATTCTGTCAG | CCCCATGGTG | 1740 |
| GTGAATTCTG | TTTCTTTCCT | TTCTTAAGGC | TGGGACATGG | TGGGCATCAG | GGACTTTGTG | 1800 |
| CTAAGCCTGA | TGAAATGTGC | TCCTTCAATC | TCCATTGAAAC | CATCGTAACA | TGGAGGCCTC | 1860 |
| AGCTGCTCTG | AGGAGAGAAA | TCAGACTTTG | TTTTTTGAAA | TGCATTTGGA | TCGAAAGCCT | 1920 |
| GAAATAAATA | TTCATACTTT | CCATAGTCCA | CCCAAAATGA | GAAAGGAGGA | GAAAAAAA | 1980 |
| AAGGGGGGGG | CGCCGGCCTA | GTGACCCCTG | TCGACCCGGG | AATTAAATTC | CGGACCGGGA | 2040 |
| CCTGCAGGGG | TGTACCAGGT | TTTCCCT | | | | 2067 |

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT16
- (B) CLONE: 2792472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| cgaggaggccg | gagccaagcc | agcgaccac | catggagacc | cgctacaacc | tgaagagtcc | 60 |
| ggctgttaaa | cgtttaatga | aagaagcggc | agaattgaaa | gatccaacag | atcattacca | 120 |
| tgcgcagcct | ttagaggata | acctttttga | atggcacttc | acggtttagag | ggccccaga | 180 |
| ctccgatttt | gatggaggag | tttatcacgg | gcggatagta | ctgccaccag | agtatcccat | 240 |
| gaaaccacca | agcattattc | tcctaacggc | taatggtcga | tttgaagtgg | gcaagaaaat | 300 |
| ctgtttgagc | atctcaggcc | atcatcctga | aacttggcag | ccttcgtgga | gtataaggac | 360 |
| agcattatta | gccatcattg | ggtttatgcc | aacaaaagga | gagggagcca | taggttctct | 420 |
| agattacact | cctgaggaaa | gaagagcact | tgccaaaaaa | tcacaagatt | tctgttgtga | 480 |
| aggatgtggc | tctgccatga | aggatgtcct | gttgccctta | aaatctggaa | gcgattcaag | 540 |
| ccaagctgac | caagaagcca | aagaactggc | taggcaaata | agctttaagg | cagaagtcaa | 600 |
| ttcatctgga | aagactatct | ctgagtcaga | cttaaacacc | tctttttcac | taactgattt | 660 |
| acaagatgat | atactacaaa | cattccaggg | tgctacggcc | agtagatcgt | acggactcca | 720 |
| gaattcctca | gcagcatcct | ttcatcaacc | taccacacct | gtagctaaga | atacctccat | 780 |

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| gagccctcga | cagcgccggg | cccagcagca | gagtcagaga | aggttgtcta | cttcaccaga | 840 |
| tgtaatccag | ggccaccagc | caagagacaa | ccacactgat | catggtgggt | cagctgtact | 900 |
| gattgtcatc | ctgacttttg | cattggcagc | tcttatattc | cgacgaatat | atctggcaaa | 960 |
| cgaatacata | tttgactttg | agttataata | tggttttgtg | acttatgagc | tgtgactcaa | 1020 |
| ctgcttcatt | aaacattctg | cattgggtat | aatctaaaaa | aaaaaaa | | 1067 |

092005 091401